



1600

RAW SEQUENCE LISTING

DATE: 07/21/2003

PATENT APPLICATION: US/09/599,760B

TIME: 08:03:52

Input Set : A:\V00139.70059.US seq.txt

Output Set: N:\CRF4\07212003\I599760B.raw

3 <110> APPLICANT: Newell, Martha K
 5 <120> TITLE OF INVENTION: Methods and products for manipulating uncoupling protein
 6 expression
 8 <130> FILE REFERENCE: V00139.70059.US
 10 <140> CURRENT APPLICATION NUMBER: 09/599,760B
 11 <141> CURRENT FILING DATE: 2000-06-22
 13 <150> PRIOR APPLICATION NUMBER: US 60/140,574
 14 <151> PRIOR FILING DATE: 1999-06-23

16 <160> NUMBER OF SEQ ID NOS: 19
 18 <170> SOFTWARE: PatentIn version 3.2

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 924

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <400> SEQUENCE: 1

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 28 ggaatagcgg cgtgcttggc ggacgtgac accttcccgc tggacacggc caaagtcggg 120
 30 ctccagggtcc aagggtgaatg cccgacgtcc agtggtatta ggtataaagg tgcctggga 180
 32 acaatcaccg ctgtggtaaa aacagaaggc cggatgaaac tctacagcgg gctgcctgcg 240
 34 gggcttcagc ggcaaatcag ctccgcctct ctcaggatcg gcctctacga cacgggtccag 300
 36 gagttcctca ccgcaggga agaaacagca cctagtttag gaagcaagat tttagctggg 360
 38 ctaacgactg gaggagtggc agtattcatt gggcaaccca cagaggtcgt gaaagtcaga 420
 40 cttcaagcac agagccatct ccacggaatc aaacctcgct acacggggac ttataatgcg 480
 42 tacagaataa tagcaacaac cgaaggcttg acgggtcttt ggaaaggac tactcccaat 540
 44 ctgatgagaa gtgtcatcat caattgtaca gagctagtaa catatgatct aatgaaggag 600
 46 gcctttgtga aaaacaacat attagcagat gacgtcccct gccacttggg gtcggctctt 660
 48 atcgctggat tttgcgcaac agctatgtcc tccccgggtg atgtagtaaa aaccagattt 720
 50 attaattctc caccaggaca gtacaaaagt gtgcccact gtgcaatgaa agtggttact 780
 52 aacgaaggac caacggcttt cttcaagggg ttggtacctt ccttcttgcg acttgatcc 840
 54 tggaacgtca ttatgtttgt gtgctttgaa caactgaaac gagaactgtc aaagtcaagg 900
 56 cagactatgg actgtgccac ataa 924

59 <210> SEQ ID NO: 2

60 <211> LENGTH: 307

61 <212> TYPE: PRT

62 <213> ORGANISM: Homo sapiens

64 <400> SEQUENCE: 2

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 66 1 5 10 15
 68 Leu Phe Ser Ala Gly Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe
 69 20 25 30
 71 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro
 72 35 40 45
 74 Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala

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75      50      55      60
77 Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala
78 65      70      75      80
80 Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr
81      85      90      95
83 Asp Thr Val Gln Glu Phe Leu Thr Ala Gly Lys Glu Thr Ala Pro Ser
84      100      105      110
86 Leu Gly Ser Lys Ile Leu Ala Gly Leu Thr Thr Gly Gly Val Ala Val
87      115      120      125
89 Phe Ile Gly Gln Pro Thr Glu Val Val Lys Val Arg Leu Gln Ala Gln
90      130      135      140
92 Ser His Leu His Gly Ile Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala
93 145      150      155      160
95 Tyr Arg Ile Ile Ala Thr Thr Glu Gly Leu Thr Gly Leu Trp Lys Gly
96      165      170      175
98 Thr Thr Pro Asn Leu Met Arg Ser Val Ile Ile Asn Cys Thr Glu Leu
99      180      185      190
101 Val Thr Tyr Asp Leu Met Lys Glu Ala Phe Val Lys Asn Asn Ile Leu
102      195      200      205
104 Ala Asp Asp Val Pro Cys His Leu Val Ser Ala Leu Ile Ala Gly Phe
105      210      215      220
107 Cys Ala Thr Ala Met Ser Ser Pro Val Asp Val Val Lys Thr Arg Phe
108 225      230      235      240
110 Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val Pro Asn Cys Ala Met
111      245      250      255
113 Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe Phe Lys Gly Leu Val
114      260      265      270
117 Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Ile Met Phe Val Cys
118      275      280      285
120 Phe Glu Gln Leu Lys Arg Glu Leu Ser Lys Ser Arg Gln Thr Met Asp
121      290      295      300
123 Cys Ala Thr
124 305

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127 <210> SEQ ID NO: 3

128 <211> LENGTH: 1105

129 <212> TYPE: DNA

130 <213> ORGANISM: Homo sapiens

132 <400> SEQUENCE: 3

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133 gttcctctat ctgctcttgt tgctgattaa aggtgcccct gtctccagtt tttctccatc      60
135 tcctgggacg tagcaggaaa tcagcatcat gggtgggttc aaggccacag atgtgcccc      120
137 tactgccact gtgaagtttc ttggggctgg cacagctgcc tgcctgcag atctcatcac      180
139 ctttcctctg gatactgcta aagtcgggtt acagatccaa ggagaaagtc agggggccagt      240
141 gcgcgtaca gccagcgccc agtaccggg tgtgatgggc accattctga ccatggtgcg      300
143 tactgagggc cccgaagcc tctacaatgg gctggttgcc ggctgcagc gccaaatgag      360
145 ctttgccctc gtccgcctcg gcctgtatga ttctgtcaaa cagttctaca ccaagggtc      420
147 tgagcatgcc agcattggga gccgcctcct agcaggcagc accacaggtg ccctggctgt      480
149 ggctgtggcc cagcccacgg atgtggttaa ggtccgattc caagtcagg cccgggctgg      540
151 aggtggtcgg agataccaaa gcaccgtcaa tgctacaag accattgcc gagaggaagg      600
153 gttccggggc ctctggaaag ggacctctcc caatgttgct cgtaatgcca ttgtcaactg      660

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155 tgctgagctg gtgacctatg acctcatcaa ggatgccctc ctgaaagcca acctcatgac 720
157 agatgacctc ccttgccact tcaattctgc ctttggggca ggcttctgca ccactgtcat 780
159 cgctccctt gtagacgtgg tcaagacgag atacatgaac tctgccctgg gccagtacag 840
161 tagcgctggc cactgtgccc ttaccatgct ccagaaggag gggccccgag ctttctacaa 900
163 agggttcatg ccttcctttc tccgcttggg ttcttggaaac gtggtgatgt tcgtcaccta 960
165 tgagcagctg aaacgagccc tcatggctgc ctgcacttcc cgagaggctc ctttctgagc 1020
167 ctctcctgct gctgacctga tcacctctgg ctttgtctct agccggggcca tgctttcctt 1080
169 ttcttccttc tttctcttcc ctccg 1105
172 <210> SEQ ID NO: 4
173 <211> LENGTH: 309
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 4
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179 1 5 10 15
181 Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe
182 20 25 30
184 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
185 35 40 45
187 Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly
188 50 55 60
190 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
191 65 70 75 80
193 Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
194 85 90 95
196 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
197 100 105 110
199 His Ala Ser Ile Gly Ser Arg Leu Ala Gly Ser Thr Thr Gly Ala
200 115 120 125
202 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
203 130 135 140
205 Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val
206 145 150 155 160
208 Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp
209 165 170 175
211 Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
212 180 185 190
214 Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
215 195 200 205
217 Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
218 210 215 220
220 Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
221 225 230 235 240
223 Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
224 245 250 255
226 Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
227 260 265 270
229 Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
230 275 280 285

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235 Arg Glu Ala Pro Phe
236 305
239 <210> SEQ ID NO: 5
240 <211> LENGTH: 1132
241 <212> TYPE: DNA
242 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 5
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247 ccaccgctgc actgaagccc agggctgtgg ageagcctct ctccttggac ctcctctcgg      120
249 ccctaaaggg actgggcaga gccttccagg actatggttg gactgaagcc ttcagacgtg      180
251 cctcccacca tggctgtgaa gttcctgggg gcaggcacag cagcctgttt tgctgacctc      240
253 gttacctttc cactggacac agccaaggtc cgcctgcaga tccaggggga gaaccaggcg      300
255 gtccagacgg ccgggtcgtg gcagtaccgt ggcgtgctgg gcaccatcct gaccatgggtg      360
257 cggactgagg gtccctgcag cccctacaat gggctggtgg ccggcctgca gcgccagatg      420
259 agcttcgcct ccatccgcat cggcctctat gactccgtca agcagggtga ccccccaaa      480
261 ggcgcggaca actccagcct cactaccggg attttggccg gctgcaccac aggagccatg      540
263 gcggtgacct gtgccagccc cacagatgtg gtgaagggtc gatttcaggc cagcatacac      600
265 ctcgggccat ccaggagcga cagaaaatac agcgggacta tggacgccta cagaaccatc      660
267 gccaggggagg aaggagtcag gggcctgtgg aaaggaactt tgcccaacat catgaggaat      720
269 gctatcgtca actgtgctga ggtggtgacc tacgacatcc tcaaggagaa gctgctggac      780
271 taccacctgc tcactgacaa cttcccctgc cactttgtct ctgcctttgg agccggcttc      840
273 tgtgccacag tgggtggcctc cccgggtggac gtggtgaaga cccgggtatat gaactcacct      900
275 ccaggccagt acttcagccc cctcgactgt atgataaaga tgggtggccca ggagggcccc      960
277 acagccttct acaaggggtg agcctcctcc tgcctccagc actccctccc agagaacagg      1020
279 ggcttctttc ttttcgaatg tggctaccgt gggtaacctt gggatgtagc ggtgaagagt      1080
281 acagatgtaa atgccacaaa gaagaagttt aaaaaacat gcaaaaaaaaa aa      1132
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 275
286 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
289 <400> SEQUENCE: 6
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291 1                      5                      10                      15
293 Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe
294      20                      25                      30
296 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln
297      35                      40                      45
299 Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr
300      50                      55                      60
302 Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly
303 65                      70                      75                      80
305 Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile
306      85                      90                      95
308 Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp
309      100                     105                     110
311 Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala
312      115                     120                     125

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314 Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
315      130      135      140
317 Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser
318 145      150      155      160
320 Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg
321      165      170      175
323 Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val
324      180      185      190
326 Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu
327      195      200      205
329 Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala
330      210      215      220
332 Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val
333 225      230      235      240
335 Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro
336      245      250      255
338 Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe
339      260      265      270
341 Tyr Lys Gly
342      275
345 <210> SEQ ID NO: 7
346 <211> LENGTH: 25
347 <212> TYPE: PRT
348 <213> ORGANISM: Unknown
350 <220> FEATURE:
352 <223> OTHER INFORMATION: P-Cadherin membrane attachment domain
354 <400> SEQUENCE: 7
355 Phe Ile Leu Pro Ile Leu Gly Ala Val Leu Ala Leu Leu Leu Leu Leu
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358 Thr Leu Leu Ala Leu Leu Leu Leu Val
359      20      25
362 <210> SEQ ID NO: 8
363 <211> LENGTH: 26
364 <212> TYPE: PRT
365 <213> ORGANISM: Unknown
367 <220> FEATURE:
369 <223> OTHER INFORMATION: CD2 membrane attachment domain
371 <400> SEQUENCE: 8
372 Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met Val
373 1      5      10      15
375 Phe Val Ala Leu Leu Val Phe Tyr Ile Thr
376      20      25
379 <210> SEQ ID NO: 9
380 <211> LENGTH: 22
381 <212> TYPE: PRT
382 <213> ORGANISM: Unknown
384 <220> FEATURE:
386 <223> OTHER INFORMATION: CD40 membrane attachment domain
388 <400> SEQUENCE: 9

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VERIFICATION SUMMARY

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